



-1-

SEQUENCE LISTING

<110> Gardella, Thomas J.
Kronenberg, Henry M.
Potts, John T.
Juppner, Harald

<120> PTH Functional Domain Conjugate Peptides, Derivatives
Thereof and Novel Tethered Ligand-Receptor Molecules

<130> 0609.4780001

<140> US 09/475,158

<141> 1999-12-30

<150> US 60/114,577

<151> 1998-12-31

<160> 67

<170> PatentIn Ver. 2.1

<210> 1

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1

Ala Val Ser Glu Ile Gln Leu Met His
1 5

<210> 2

<211> 17

<212> PRT

<213> Homo sapiens

<400> 2

Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp
1 5 10 15

Val

<210> 3

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
sequence

<400> 3

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 4
<211> 5
<212> PRT
<213> Homo sapiens

<400> 4
Ala Val Ser Glu Ile
1 5

<210> 5
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 5
Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Gly Gly Leu Asn
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 6
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 6
Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 7
<211> 9
<212> PRT
<213> Homo sapiens

<400> 7
Ala Val Ser Glu His Gln Leu Leu His
1 5

<210> 8
<211> 17
<212> PRT
<213> Homo sapiens

<400> 8
Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu
1 5 10 15

Ile

<210> 9
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 9
Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Leu Asn
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 10
<211> 5
<212> PRT
<213> Homo sapiens

<400> 10
Ala Val Ser Glu His
1 5

<210> 11
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 11
Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 12
<211> 15
<212> PRT
<213> Homo sapiens

<400> 12
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
1 5 10 15

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 13
Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Gly Gly Leu Asn
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 14
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 14
gcuguuuccg aaauccagcu gaugcacggu ggugguggug gucugaacuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 15
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 15
gcuguuuccg aaauccagcu gaugcacggu ggugguggug guggugguuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 16
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 16
gcuguuuccg aaauccgugg uggugguggu ggugguggug gucugaacuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 17
<211> 34
<212> PRT
<213> Homo sapiens

<400> 17
Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
 20 25 30

Asn Phe

<210> 18
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 18
 Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln
 1 5 10 15
 Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile His
 20 25 30

Thr Ala

<210> 19
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 19
 His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
 1 5 10 15
 Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys
 20 25 30

Gln Arg Val Asn Lys
 35

<210> 20
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 20
 His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln
 1 5 10 15
 Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Leu Asn
 20 25

<210> 21
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 21
 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
 1 5 10 15
 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg

20

25

<210> 22
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 22
 His Ala Asp Gly Val Phe Thr Ser Asp Phe Ser Lys Leu Leu Gly Gln
 1 5 10 15
 Leu Ser Ala Lys Lys Tyr Leu Glu Ser Leu Met
 20 25

<210> 23
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 23
 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 1 5 10 15
 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 20 25 30

<210> 24
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 24
 His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser
 1 5 10 15
 Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
 20 25

<210> 25
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 25
 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys
 1 5 10 15
 Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys Gly Lys
 20 25 30
 Lys Asn Asp Trp Lys His Asn Ile Thr Gln
 35 40

<210> 26
 <211> 27
 <212> PRT

<213> Homo sapiens

<400> 26

His Ser Asp Gly Thr Phe Thr Ser Glu Leu Ser Arg Leu Arg Glu Gly
1 5 10 15

Ala Arg Leu Gln Arg Leu Leu Gln Gly Leu Val
20 25

<210> 27

<211> 32

<212> PRT

<213> Homo sapiens

<400> 27

Cys Gly Asn Leu Ser Thr Cys Met Leu Gly Thr Tyr Thr Gln Asp Phe
1 5 10 15

Asn Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro
20 25 30

<210> 28

<211> 37

<212> PRT

<213> Homo sapiens

<400> 28

Ala Cys Asn Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu
1 5 10 15

Ser Arg Ser Gly Gly Met Val Lys Ser Asn Phe Val Pro Thr Asn Val
20 25 30

Gly Ser Lys Ala Phe
35

<210> 29

<211> 37

<212> PRT

<213> Homo sapiens

<400> 29

Ala Cys Asp Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu
1 5 10 15

Ser Arg Ser Gly Gly Val Val Lys Asn Asn Phe Val Pro Thr Asn Val
20 25 30

Gly Ser Lys Ala Phe
35

<210> 30

<211> 37

<212> PRT

<213> Homo sapiens

<400> 30
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
 1 5 10 15
 Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val
 20 25 30
 Gly Ser Asn Thr Tyr
 35

<210> 31
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 31
 Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile
 1 5 10 15
 Tyr Gln Phe Thr Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys
 20 25 30
 Ile Ser Pro Gln
 35

<210> 32
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 32
 Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg
 1 5 10 15
 Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His
 20 25 30
 Ser Asn Arg Lys Leu Met Glu Ile Ile
 35 40

<210> 33
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 33
 Glu Glu Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys
 1 5 10 15
 Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn
 20 25 30
 Asn Arg Leu Leu Leu Asp Thr Ile
 35 40

<210> 34
 <211> 46
 <212> PRT

<213> Homo sapiens

<400> 34

Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
 1 5 10 15
 Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln
 20 25 30
 Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
 35 40 45

<210> 35

<211> 63

<212> PRT

<213> Homo sapiens

<400> 35

Cys Asp Ala Thr Cys Gln Phe Arg Lys Ala Ile Asp Asp Cys Gln Lys
 1 5 10 15
 Gln Ala His His Ser Asn Val Leu Gln Thr Ser Val Gln Thr Thr Ala
 20 25 30
 Thr Phe Thr Ser Met Asp Thr Ser Gln Leu Pro Gly Asn Ser Val Phe
 35 40 45
 Lys Glu Cys Met Lys Gln Lys Lys Lys Glu Phe Ser Ser Gly Lys
 50 55 60

<210> 36

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>

<221> CDS

<222> (1)..(1332)

<400> 36

atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96
 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac 144
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat 192
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60

| | |
|---|-----|
| ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac atg ttc | 240 |
| Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe | |
| 65 70 75 80 | |
| ctg tcg ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg | 288 |
| Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val | |
| 85 90 95 | |
| ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa | 336 |
| Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu | |
| 100 105 110 | |
| gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc | 384 |
| Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala | |
| 115 120 125 | |
| gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc | 432 |
| Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe | |
| 130 135 140 | |
| ctg gct acc aac tac tac tgg atc ctg gtg gag ggg ctg tac ttg cac | 480 |
| Leu Ala Thr Asn Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His | |
| 145 150 155 160 | |
| agc ctc atc ttc atg gcc ttt ttc tca gag aag aag tac ctg tgg ggc | 528 |
| Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly | |
| 165 170 175 | |
| ttc acc atc ttt ggc tgg ggt cta ccg gct gtc ttc gtg gct gtg tgg | 576 |
| Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp | |
| 180 185 190 | |
| gtc ggt gtc aga gca acc ttg gcc aac act ggg tgc tgg gat ctg agc | 624 |
| Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser | |
| 195 200 205 | |
| tcc ggg cac aag aag tgg atc atc cag gtg ccc atc ctg gca tct gtt | 672 |
| Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val | |
| 210 215 220 | |
| gtg ctc aac ttc atc ctt ttt atc aac atc atc cgg gtg ctt gcc act | 720 |
| Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr | |
| 225 230 235 240 | |
| aag ctt cgg gag acc aat gcg ggc cgg tgt gac acc agg cag cag tac | 768 |
| Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr | |
| 245 250 255 | |
| cgg aag ctg ctc agg tcc acg ttg gtg ctc gtg ccg ctc ttt ggt gtg | 816 |
| Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val | |
| 260 265 270 | |
| cac tac acc gtc ttc atg gcc ttg ccg tac acc gag gtc tca ggg aca | 864 |
| His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr | |
| 275 280 285 | |
| ttg tgg cag atc cag atg cat tat gag atg ctc ttc aac tcc ttc cag | 912 |
| Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln | |
| 290 295 300 | |
| gga ttt ttt gtt gcc atc ata tac tgt ttc tgc aat ggt gag gtg cag | 960 |
| Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln | |

| 305 | 310 | 315 | 320 | |
|---|-----|-----|-----|------|
| gca gag att agg aag tca tgg agc cgc tgg aca ctg gcg ttg gac ttc | | | | 1008 |
| Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe | | | | |
| | 325 | 330 | 335 | |
| aag cgc aaa gca cga agt ggg agt agc agc tac agc tat ggc cca atg | | | | 1056 |
| Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met | | | | |
| | 340 | 345 | 350 | |
| gtg tct cac acg agt gtg acc aat gtg ggc ccc cgt gca gga ctc agc | | | | 1104 |
| Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser | | | | |
| | 355 | 360 | 365 | |
| ctc ccc ctc agc ccc cgc ctg cct cct gcc act acc aat ggc cac tcc | | | | 1152 |
| Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser | | | | |
| | 370 | 375 | 380 | |
| cag ctg cct ggc cat gcc aag cca ggg gct cca gcc act gag act gaa | | | | 1200 |
| Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu | | | | |
| | 385 | 390 | 395 | 400 |
| acc cta cca gtc act atg gcg gtt ccc aag gac gat gga ttc ctt aac | | | | 1248 |
| Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn | | | | |
| | 405 | 410 | 415 | |
| ggc tcc tgc tca ggc ctg gat gag gag gcc tcc ggg tct gcg cgg ccg | | | | 1296 |
| Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro | | | | |
| | 420 | 425 | 430 | |
| cct cca ttg ttg cag gaa gga tgg gaa aca gtc atg tga | | | | 1335 |
| Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met | | | | |
| | 435 | 440 | | |

<210> 37
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 37
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
 65 70 75 80
 Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
 85 90 95
 Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
 100 105 110
 Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Ala Ala Ala Ala
 115 120 125

Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
 130 135 140
 Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
 145 150 155 160
 Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
 165 170 175
 Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
 180 185 190
 Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
 195 200 205
 Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
 210 215 220
 Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
 225 230 235 240
 Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
 245 250 255
 Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
 260 265 270
 His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr
 275 280 285
 Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln
 290 295 300
 Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln
 305 310 315 320
 Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe
 325 330 335
 Lys Arg Lys Ala Arg Ser Gly Ser Ser Tyr Ser Tyr Gly Pro Met
 340 345 350
 Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser
 355 360 365
 Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser
 370 375 380
 Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu
 385 390 395 400
 Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn
 405 410 415
 Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro
 420 425 430
 Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met
 435 440

<210> 38
 <211> 1002
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1002)

<400> 38
 atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96

| | |
|---|-----|
| Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly | |
| 20 25 30 | |
| gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac | 144 |
| Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr | |
| 35 40 45 | |
| tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat | 192 |
| Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr | |
| 50 55 60 | |
| ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac atg ttc | 240 |
| Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe | |
| 65 70 75 80 | |
| ctg tgc ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg | 288 |
| Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val | |
| 85 90 95 | |
| ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa | 336 |
| Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu | |
| 100 105 110 | |
| gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc | 384 |
| Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala | |
| 115 120 125 | |
| gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc | 432 |
| Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe | |
| 130 135 140 | |
| ctg gct acc aac tac tac tgg atc ctg gtg gag ggg ctg tac ttg cac | 480 |
| Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His | |
| 145 150 155 160 | |
| agc ctc atc ttc atg gcc ttt ttc tca gag aag aag tac ctg tgg gcc | 528 |
| Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly | |
| 165 170 175 | |
| ttc acc atc ttt ggc tgg ggt cta ccg gct gtc ttc gtg gct gtg tgg | 576 |
| Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp | |
| 180 185 190 | |
| gtc ggt gtc aga gca acc ttg gcc aac act ggg tgc tgg gat ctg agc | 624 |
| Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser | |
| 195 200 205 | |
| tcc ggg cac aag aag tgg atc atc cag gtg ccc atc ctg gca tct gtt | 672 |
| Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val | |
| 210 215 220 | |
| gtg ctc aac ttc atc ctt ttt atc aac atc atc cgg gtg ctt gcc act | 720 |
| Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr | |
| 225 230 235 240 | |
| aag ctt cgg gag acc aat gcg ggc cgg tgt gac acc agg cag cag tac | 768 |
| Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr | |
| 245 250 255 | |
| cgg aag ctg ctc agg tcc acg ttg gtg ctc gtg ccg ctc ttt ggt gtg | 816 |
| Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val | |
| 260 265 270 | |

| | |
|---|------|
| cac tac acc gtc ttc atg gcc ttg ccg tac acc gag gtc tca ggg aca | 864 |
| His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr | |
| 275 280 285 | |
| ttg tgg cag atc cag atg cat tat gag atg ctc ttc aac tcc ttc cag | 912 |
| Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln | |
| 290 295 300 | |
| gga ttt ttt gtt gcc atc ata tac tgt ttc tgc aat ggt gag gtg cag | 960 |
| Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln | |
| 305 310 315 320 | |
| gca gag att agg aag tca tgg agc cgc tgg aca ctg gcg tag | 1002 |
| Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala | |
| 325 330 | |

<210> 39
 <211> 333
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 39
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
 65 70 75 80
 Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
 85 90 95
 Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
 100 105 110
 Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala
 115 120 125
 Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
 130 135 140
 Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
 145 150 155 160
 Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
 165 170 175
 Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
 180 185 190
 Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
 195 200 205
 Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
 210 215 220
 Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
 225 230 235 240
 Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
 245 250 255
 Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
 260 265 270

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Tyr | Thr | Val | Phe | Met | Ala | Leu | Pro | Tyr | Thr | Glu | Val | Ser | Gly | Thr |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Leu | Trp | Gln | Ile | Gln | Met | His | Tyr | Glu | Met | Leu | Phe | Asn | Ser | Phe | Gln |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Gly | Phe | Phe | Val | Ala | Ile | Ile | Tyr | Cys | Phe | Cys | Asn | Gly | Glu | Val | Gln |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ala | Glu | Ile | Arg | Lys | Ser | Trp | Ser | Arg | Trp | Thr | Leu | Ala | | | |
| | | | | 325 | | | | | 330 | | | | | | |

<210> 40
 <211> 975
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(972)

| | |
|---|-----|
| <400> 40 | |
| atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc | 48 |
| Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys | |
| 1 5 10 15 | |
| cca gtg ctc agc tcc gca tat gcg ctg gag gta ttt gac cgc cta ggc | 96 |
| Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly | |
| 20 25 30 | |
| atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg | 144 |
| Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val | |
| 35 40 45 | |
| gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac | 192 |
| Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn | |
| 50 55 60 | |
| tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc | 240 |
| Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser | |
| 65 70 75 80 | |
| atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag | 288 |
| Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu | |
| 85 90 95 | |
| gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca | 336 |
| Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro | |
| 100 105 110 | |
| cct ccg ccg gcc gct gcc gcc gta ggc tac gct ggc tgc cgc gtg gcg | 384 |
| Pro Pro Pro Ala Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala | |
| 115 120 125 | |
| gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg | 432 |
| Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu | |
| 130 135 140 | |

| | |
|---|-----|
| gtg gag ggg ctg tac ttg cac agc ctc atc ttc atg gcc ttt ttc tca | 480 |
| Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser | |
| 145 150 155 160 | |
| gag aag aag tac ctg tgg ggc ttc acc atc ttt ggc tgg ggt cta ccg | 528 |
| Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro | |
| 165 170 175 | |
| gct gtc ttc gtg gct gtg tgg gtc ggt gtc aga gca acc ttg gcc aac | 576 |
| Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn | |
| 180 185 190 | |
| act ggg tgc tgg gat ctg agc tcc ggg cac aag aag tgg atc atc cag | 624 |
| Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln | |
| 195 200 205 | |
| gtg ccc atc ctg gca tct gtt gtg ctc aac ttc atc ctt ttt atc aac | 672 |
| Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn | |
| 210 215 220 | |
| atc atc cgg gtg ctt gcc act aag ctt cgg gag acc aat gcg ggc cgg | 720 |
| Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg | |
| 225 230 235 240 | |
| tgt gac acc agg cag cag tac cgg aag ctg ctc agg tcc acg ttg gtg | 768 |
| Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val | |
| 245 250 255 | |
| ctc gtg ccg ctc ttt ggt gtg cac tac acc gtc ttc atg gcc ttg ccg | 816 |
| Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro | |
| 260 265 270 | |
| tac acc gag gtc tca ggg aca ttg tgg cag atc cag atg cat tat gag | 864 |
| Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu | |
| 275 280 285 | |
| atg ctc ttc aac tcc ttc cag gga ttt ttt gtt gcc atc ata tac tgt | 912 |
| Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys | |
| 290 295 300 | |
| ttc tgc aat ggt gag gtg cag gca gag att agg aag tca tgg agc cgc | 960 |
| Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg | |
| 305 310 315 320 | |
| tgg aca ctg gcg tag | 975 |
| Trp Thr Leu Ala | |

<210> 41
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 41
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly

[illegible]

```
<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence
```

```
<220>
<221> UNSURE
<222> (1)..(1)
<223> May be any amino acid.
```

```
<220>  
<221> UNSURE  
<222> (3)..(3)  
<223> May be any amino acid.
```

```
<220>  
<221> UNSURE  
<222> (5)..(8)  
<223> May be any amino acid.
```

$\langle 220 \rangle$

<223> Description of Artificial Sequence: synthetic polypeptide

<400> 42
Xaa Val Xaa Glu Xaa Xaa Xaa Xaa His
1 5

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)..(5)
<223> May be any amino acid.

<220>
<221> UNSURE
<222> (7)..(8)
<223> May be any amino acid.

<220>
<221> UNSURE
<222> (10)
<223> May be any amino acid.

<220>
<221> UNSURE
<222> (12)
<223> May be any amino acid.

<220>
<221> UNSURE
<222> (15)..(16)
<223> May be any amino acid.

<220>
<223> Description of Artificial Sequence: synthetic Polypeptide

<400> 43
Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Trp Xaa Leu Xaa Lys Leu Xaa Xaa
1 5 10 15

Val

<210> 44
<211> 9
<212> PRT
<213> Homo sapiens

<400> 44
Ser Val Ser Glu Ile Gln Leu Met His
1 5

<210> 45

<211> 17
<212> PRT
<213> Homo sapiens

<400> 45
Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln
1 5 10 15

Asp Val

<210> 46
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 46
atgggggccc cccggatcgc acccagcctg gcgctcctac tctgctgccc agtgctcagc 60
tccgcatatg cgctggtgga tgcggacgat gtctttacca aagaggaaca gattttcctg 120

<210> 47
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 47
aaccggacgt gggccaacta cagcgagtgc ctcaagttca tgaccaatga gaccgaggaa 60
cgggaggtat ttgaccgcct aggcgatgatc tacaccgtgg gatactccat gtctctcgcc 120

<210> 48
<211> 39
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 48
gcguuuuccg aaauccagcu gaugcacggc ggaggaggc

39

<210> 49
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 49

ctctgctgcc cagtgtcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac 99

<210> 50
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 50
ctctgctgcc cagtgtcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac 99

<210> 51
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 51
ctctgctgcc cagtgtcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac 96

<210> 52
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 52
ctctgctgcc cagtgtcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac 96

<210> 53
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 53
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys
1 5 10 15
Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe
20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu
35 40

<210> 54
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 54
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn
1 5 10 15
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
20 25 30
Val Gly Tyr Ser Met Ser Leu Ala
35 40

<210> 55
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 55
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln
1 5 10 15
Leu Met His Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile
20 25 30
Tyr

<210> 56
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 56
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp
1 5 10 15
Tyr Ala Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
20 25 30

<210> 57
 <211> 1380
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1353)

<400> 57
 atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc 48
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys
 1 5 10 15
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cat 96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30
 aat cgt ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac 144
 Asn Arg Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
 35 40 45
 acc gtg ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc 192
 Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu
 50 55 60
 atc ctg gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac 240
 Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His
 65 70 75 80
 atg cac ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc 288
 Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val
 85 90 95
 aag gac gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc 336
 Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg
 100 105 110
 ctc acc gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct 384
 Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro
 115 120 125
 gcc acc gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc 432
 Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe
 130 135 140
 ttc ctt tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg 480
 Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly
 145 150 155 160
 ctg tac ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag 528
 Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys
 165 170 175
 tac ctg tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc 576
 Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe
 180 185 190

| | |
|---|------|
| gtg gct gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys 195 200 205 | 624 |
| tgg gac ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile 210 215 220 | 672 |
| ctg gcc tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg 225 230 235 240 | 720 |
| gtg ctc gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr 245 250 255 | 768 |
| cgg cag cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro 260 265 270 | 816 |
| ctc ttt ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu 275 280 285 | 864 |
| gtc tca ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe 290 295 300 | 912 |
| aac tcc ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn 305 310 315 320 | 960 |
| ggc gag gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu 325 330 335 | 1008 |
| gca ctg gac ttc aag cga aag gca cgc agc ggc agc agc agc tat agc Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser 340 345 350 | 1056 |
| tac ggc ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg 355 360 365 | 1104 |
| gtg gga ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr 370 375 380 | 1152 |
| acc aac ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro 385 390 395 400 | 1200 |
| gcc ctg gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys 405 410 415 | 1248 |
| gac gat ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala 420 425 430 | 1296 |
| tct ggg cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr 435 440 445 | 1344 |

435 440 445 1380
gtc atg tga ccaggcgctg ggggctggac ctgctga
Val Met
450

<210> 58
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 58
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
1 5 10 15
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
20 25 30
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
35 40 45
Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu
50 55 60
Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His
65 70 75 80
Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val
85 90 95
Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg
100 105 110
Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro
115 120 125
Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe
130 135 140
Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly
145 150 155 160
Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys
165 170 175
Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe
180 185 190
Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys
195 200 205
Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile
210 215 220
Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg
225 230 235 240
Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr
245 250 255
Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro
260 265 270
Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu
275 280 285
Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe
290 295 300
Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn
305 310 315 320
Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu
325 330 335
Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser
340 345 350
Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| | | 355 | | | | | 360 | | | | | 365 | | | | | | | |
| Val | Gly | Leu | Gly | Leu | Pro | Leu | Ser | Pro | Arg | Leu | Leu | Pro | Thr | Ala | Thr | | | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | | | |
| Thr | Asn | Gly | His | Pro | Gln | Leu | Pro | Gly | His | Ala | Lys | Pro | Gly | Thr | Pro | | | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | | | |
| Ala | Leu | Glu | Thr | Leu | Glu | Thr | Thr | Pro | Pro | Ala | Met | Ala | Ala | Pro | Lys | | | | |
| | | | | 405 | | | | | | 410 | | | | 415 | | | | | |
| Asp | Asp | Gly | Phe | Leu | Asn | Gly | Ser | Cys | Ser | Gly | Leu | Asp | Glu | Glu | Ala | | | | |
| | | 420 | | | | | | 425 | | | | | 430 | | | | | | |
| Ser | Gly | Pro | Glu | Arg | Pro | Pro | Ala | Leu | Leu | Gln | Glu | Glu | Trp | Glu | Thr | | | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | | | |
| Val | Met | | | | | | | | | | | | | | | | | | |
| | 450 | | | | | | | | | | | | | | | | | | |

<210> 59
 <211> 1380
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (28)..(1335)

<400> 59
 tggatcccg gcgcctaggc ggtggcg atg ggg acc gcc cgg atc gca ccc ggc 54
 Met Gly Thr Ala Arg Ile Ala Pro Gly
 1 5

ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gca tat gag gtg 102
 Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Glu Val
 10 15 20 25

ttt gac cgc ctg ggc atg att tac acc gtg ggc tac tcc gtg tcc ctg 150
 Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu
 30 35 40

gcg tcc ctc acc gta gct gtg ctc atc ctg gcc tac ttt agg cgg ctg 198
 Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu
 45 50 55

cac tgc acg cgc aac tac atc cac atg cac ctg ttc ctg tcc ttc atg 246
 His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met
 60 65 70

ctg cgc gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc 294
 Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly
 75 80 85

gcc acg ctt gat gag gct gag cgc ctc acc gag gag gag ctg cgc gcc 342
 Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala
 90 95 100 105

atc gcc cag gcg ccc ccg ccg cct gcc acc gcc gct gcc ggc tac gcg 390
 Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala
 110 115 120

| | |
|---|------|
| ggc tgc agg gtg gct gtg acc ttc ttc ctt tac ttc ctg gcc acc aac Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn 125 130 135 | 438 |
| tac tac tgg att ctg gtg gag ggg ctg tac ctg cac agc ctc atc ttc Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe 140 145 150 | 486 |
| atg gcc ttc ttc tca gag aag aag tac ctg tgg ggc ttc aca gtc ttc Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe 155 160 165 | 534 |
| ggc tgg ggt ctg ccc gct gtc ttc gtg gct gtg tgg gtc agt gtc aga Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg 170 175 180 185 | 582 |
| gct acc ctg gcc aac acc ggg tgc tgg gac ttg agc tcc ggg aac aaa Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys 190 195 200 | 630 |
| aag tgg atc atc cag gtg ccc atc ctg gcc tcc att gtg ctc aac ttc Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe 205 210 215 | 678 |
| atc ctc ttc atc aat atc gtc cgg gtg ctc gcc acc aag ctg cgg gag Ile Leu Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Leu Arg Glu 220 225 230 | 726 |
| acc aac gcc ggc cgg tgt gac aca cgg cag cag tac cgg aag ctg ctc Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu 235 240 245 | 774 |
| aaa tcc acg ctg gtg ctc atg ccc ctc ttt ggc gtc cac tac att gtc Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val 250 255 260 265 | 822 |
| ttc atg gcc aca cca tac acc gag gtc tca ggg acg ctc tgg caa gtc Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val 270 275 280 | 870 |
| cag atg cac tat gag atg ctc ttc aac tcc ttc cag gga ttt ttt gtc Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val 285 290 295 | 918 |
| gca atc ata tac tgt ttc tgc aat ggc gag gta caa gct gag atc aag Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys 300 305 310 | 966 |
| aaa tct tgg agc cgc tgg aca ctg gca ctg gac ttc aag cga aag gca Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala 315 320 325 | 1014 |
| cgc agc ggg agc agc agc tat agc tac ggc ccc atg gtg tcc cac aca Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr 330 335 340 345 | 1062 |
| agt gtg acc aat gtc ggc ccc cgt gtg gga ctc ggc ctg ccc ctc agc Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser 350 355 360 | 1110 |
| ccc cgc cta ctg ccc act gcc acc acc aac ggc cac cct cag ctg cct Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro | 1158 |

| | | | |
|---|-----|-----|------|
| 365 | 370 | 375 | |
| ggc cat gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca | | | 1206 |
| Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr | | | |
| 380 | 385 | 390 | |
| cca cct gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc | | | 1254 |
| Pro Pro Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser | | | |
| 395 | 400 | 405 | |
| tgc tca ggc ctg gac gag gag gcc tct ggg cct gag cgg cca cct gcc | | | 1302 |
| Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala | | | |
| 410 | 415 | 420 | 425 |
| ctg cta cag gaa gag tgg gag aca gtc atg tga ccaggcgctg ggggctggac | | | 1355 |
| Leu Leu Gln Glu Glu Trp Glu Thr Val Met | | | |
| 430 | 435 | | |
| ctgctgacat agtggatgga cagat | | | 1380 |

<210> 60
 <211> 435
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 60
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Glu Val Phe Asp Arg Leu Gly Met Ile
 20 25 30
 Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val
 35 40 45
 Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile
 50 55 60
 His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe
 65 70 75 80
 Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu
 85 90 95
 Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro
 100 105 110
 Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr
 115 120 125
 Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu
 130 135 140
 Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys
 145 150 155 160
 Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val
 165 170 175
 Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly
 180 185 190
 Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro
 195 200 205
 Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val
 210 215 220
 Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp
 225 230 235 240

Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met
 245 250 255
 Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr
 260 265 270
 Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu
 275 280 285
 Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys
 290 295 300
 Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr
 305 310 315 320
 Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr
 325 330 335
 Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro
 340 345 350
 Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala
 355 360 365
 Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr
 370 375 380
 Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro
 385 390 395 400
 Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
 405 410 415
 Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu
 420 425 430
 Thr Val Met
 435

<210> 61
 <211> 1363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1347)

<400> 61
 atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc 48
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cac 96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30
 ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac acc gtg 144
 Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val
 35 40 45
 ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc atc ctg 192
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
 50 55 60
 gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac 240
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
 65 70 75 80

| | |
|---|------|
| ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc aag gac | 288 |
| Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp | |
| 85 90 95 | |
| gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc ctc acc | 336 |
| Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr | |
| 100 105 110 | |
| gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct gcc acc | 384 |
| Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr | |
| 115 120 125 | |
| gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc ttc ctt | 432 |
| Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu | |
| 130 135 140 | |
| tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg ctg tac | 480 |
| Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr | |
| 145 150 155 160 | |
| ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag tac ctg | 528 |
| Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu | |
| 165 170 175 | |
| tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc gtg gct | 576 |
| Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala | |
| 180 185 190 | |
| gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc tgg gac | 624 |
| Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp | |
| 195 200 205 | |
| ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc ctg gcc | 672 |
| Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala | |
| 210 215 220 | |
| tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg gtg ctc | 720 |
| Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu | |
| 225 230 235 240 | |
| gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca cgg cag | 768 |
| Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln | |
| 245 250 255 | |
| cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc ctc ttt | 816 |
| Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe | |
| 260 265 270 | |
| ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag gtc tca | 864 |
| Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser | |
| 275 280 285 | |
| ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc aac tcc | 912 |
| Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser | |
| 290 295 300 | |
| ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat ggc gag | 960 |
| Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu | |
| 305 310 315 320 | |
| gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg gca ctg | 1008 |
| Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu | |

| 325 | 330 | 335 | |
|---|-----|-----|------|
| gac ttc aag cga aag gca cgc agc ggg agc agc agc tat agc tac ggc | | | 1056 |
| Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly | | | |
| 340 | 345 | 350 | |
| ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt gtg gga | | | 1104 |
| Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly | | | |
| 355 | 360 | 365 | |
| ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc acc aac | | | 1152 |
| Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn | | | |
| 370 | 375 | 380 | |
| ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca gcc ctg | | | 1200 |
| Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu | | | |
| 385 | 390 | 395 | 400 |
| gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag gac gat | | | 1248 |
| Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp | | | |
| 405 | 410 | 415 | |
| ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc tct ggg | | | 1296 |
| Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly | | | |
| 420 | 425 | 430 | |
| cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca gtc atg | | | 1344 |
| Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met | | | |
| 435 | 440 | 445 | |
| tga ccagggcgtg ggggct | | | 1363 |

<210> 62
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 62
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30
 Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val
 35 40 45
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
 50 55 60
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
 65 70 75 80
 Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp
 85 90 95
 Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr
 100 105 110
 Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Ala Thr
 115 120 125
 Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu
 130 135 140

Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr
 145 150 155 160
 Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu
 165 170 175
 Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala
 180 185 190
 Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp
 195 200 205
 Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala
 210 215 220
 Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu
 225 230 235 240
 Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln
 245 250 255
 Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
 260 265 270
 Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
 275 280 285
 Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
 290 295 300
 Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu
 305 310 315 320
 Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu
 325 330 335
 Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
 340 345 350
 Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly
 355 360 365
 Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn
 370 375 380
 Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu
 385 390 395 400
 Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp
 405 410 415
 Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly
 420 425 430
 Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met
 435 440 445

<210> 63
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 63
 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 1 5 10 15

<210> 64
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 64
 Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Ile Gln

1 5 10 15
 Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 20 25 30

<210> 65
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 65
 Ala Val Ser Glu His Gly Gly Gly Gly Gly Gly Gly Gly Ile Gln
 1 5 10 15

Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 20 25 30

<210> 66
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 66
 Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15

Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 20 25 30

<210> 67
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 67
 Ala Val Ser Glu Ile Gln Leu Met His Asn Leu
 1 5 10

Sub
 B1
 a13
 cont